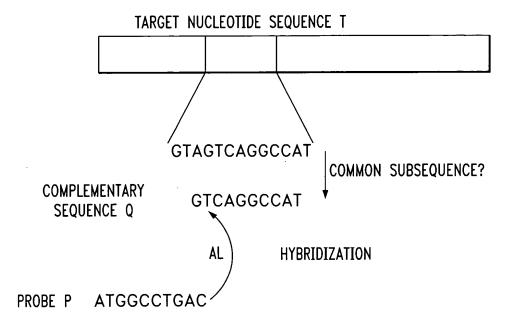
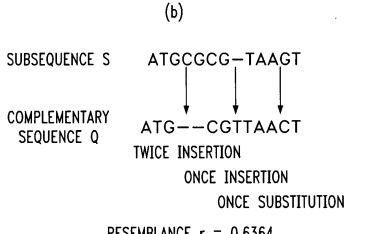


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FIG. 1

(a)





RESEMBLANCE r = 0.6364MAXIMUM EDIT DISTANCE k = 4

FIG. 2

NUCLEOTIDE SEQUENCES LIKELY TO BE CONTAINED IN SAMPLE

Q TARGET NUCLEOTIDE SEQUENCE

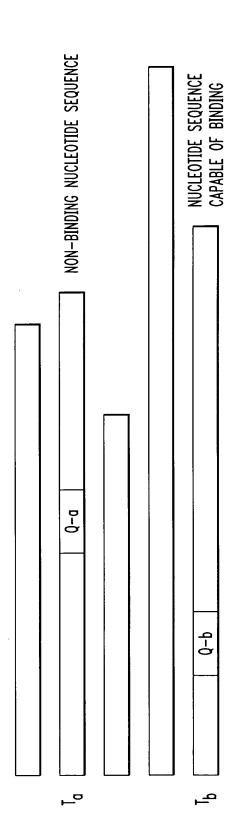


FIG. 3

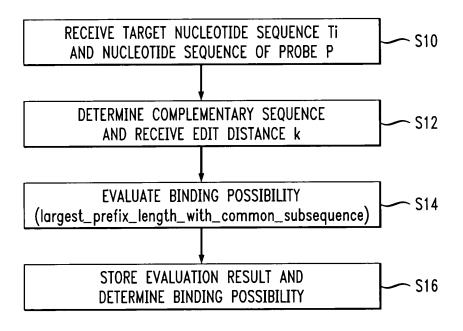
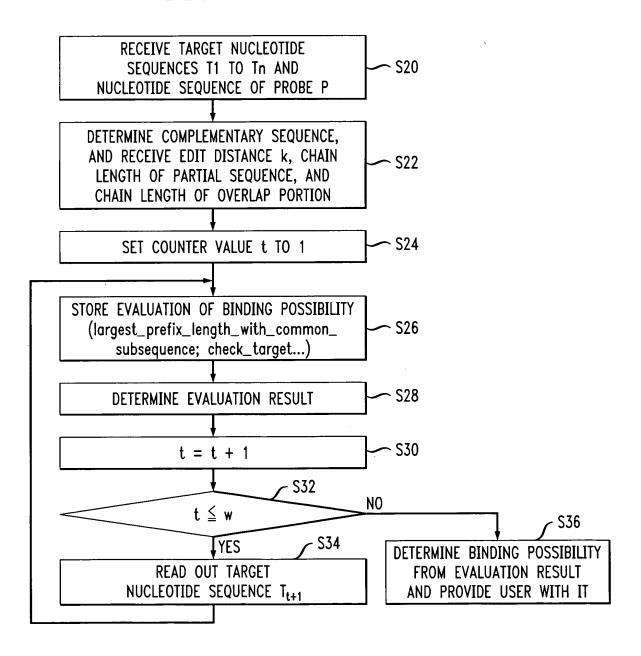
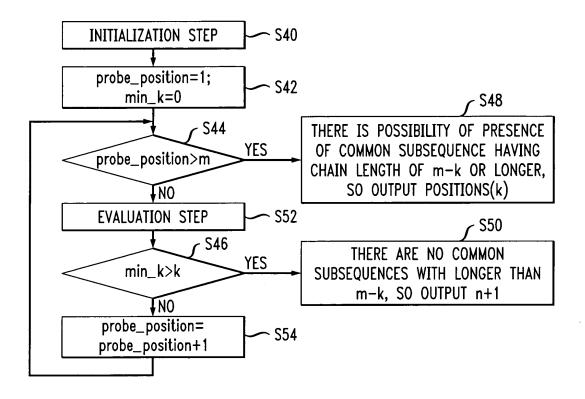
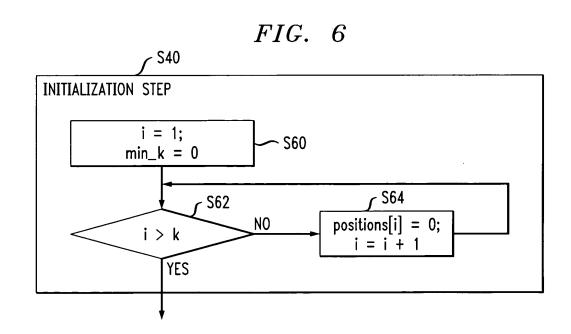


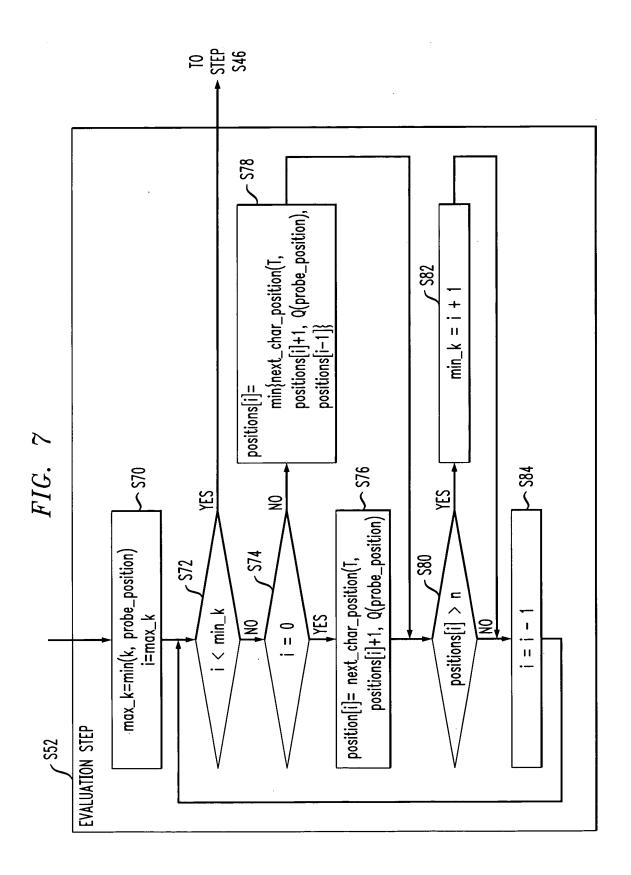
FIG. 4



 $FIG. \quad 5$ function: largest_prefix_with_common_subsequence(T,Q,k)







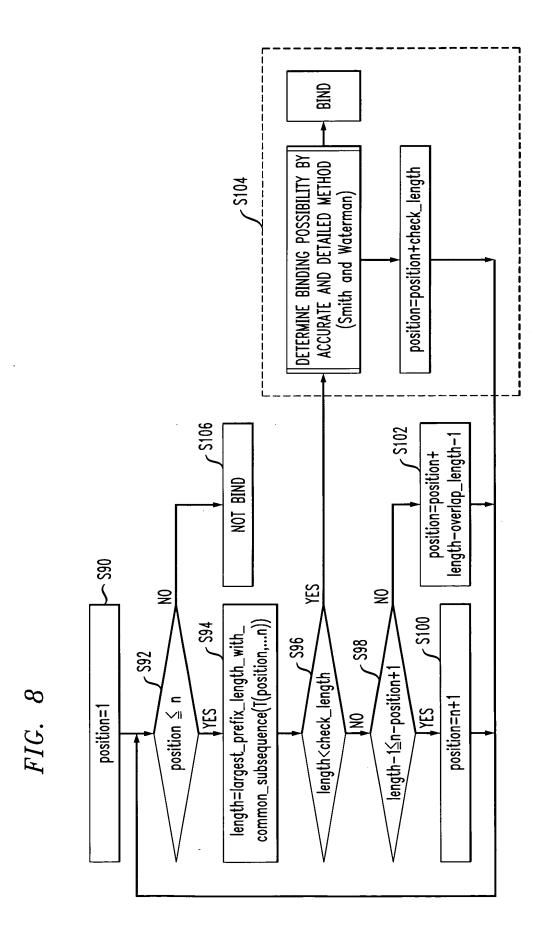


FIG. 9

```
//function largest_prefix_with_common_subsequence
largest_prefix_with_common_subsequence(sequence T[1..n], sequence Q[1..m], k) {
   for (i=0;i<=k;i++) positions[i] = 0;
   min_k = 0;
   for (probe_position=1; probe_position<=m; probe_position++) {</pre>
       max_k = min {k, probe_position};
       for (i=max_k; i>=min_k ;i--) {
           if (i==0)
                      positions[i] = next_char_position(T, positions[i]+1,
Q[probe_position]);
           } else {
                      positions[i] = min { next_char_position(T, positions[i]+1,
Q[probe_position]),
                              positions[i-1] }
           if (positions[i] > n) {
                      min_k = i+1;
       if (\min_k > k)
           1) Absence of common subsequence with length of m-k or longer
           return m+1;
   (2) Presence of common subsequence with length of m-min_k or longer
   return positions(k)
```

FIG. 10

```
//function check_target
check_target(sequence T[1..n], sequence Q[1..m],k, overlap_length, check_length) {
    position=1;
    while(position <= n) {
        length = largest_prefix_length_with_common_subsequence(
                               T[position..n], Q[1..m], k);
        if (length < check_length) {</pre>
            if (check_exactly(
                       T[position..(min(n, position+check_length))], Q, k)) {
                position = position + check_length;
            } else {
                return ("T binds to P")
        \{ else if (length -1 <= n - position + 1)<math>\}
          position = position + length - overlap_length - 1;
        { else }
          position = n+1;
    return ("T does not bind to P");
```

FIG. 11

	1	2	3	4	5	6	7	8
POSITIONS[0]	2	3	5	-	ı	-	-	ı
POSITIONS[1]	0	1	3	5	6	7	8	ı
POSITIONS[2]	_	0	1	3	5	6	7	8
POSITIONS[3]	_	-	0	1	3	5	6	7

FIG. 12

[positions[1],m]= (positions[1], 1, 3, 5, 6, 7, 8)

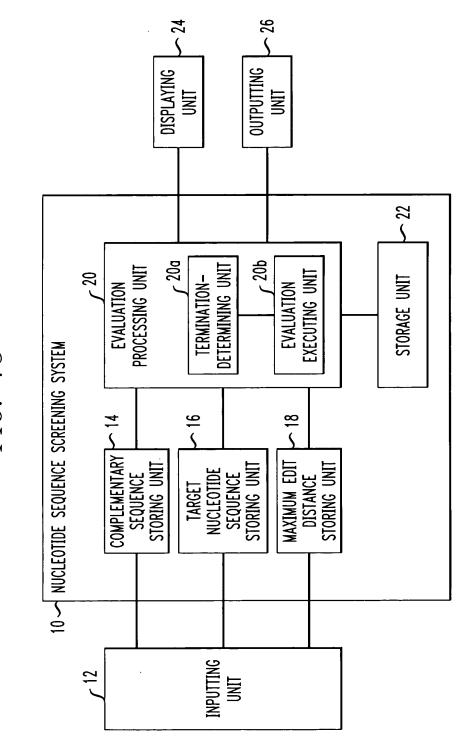


FIG. 13

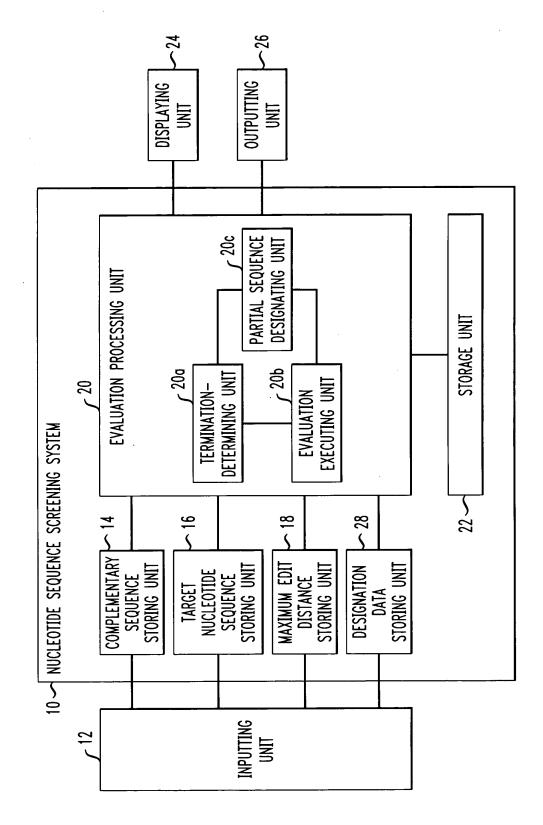


FIG. 14

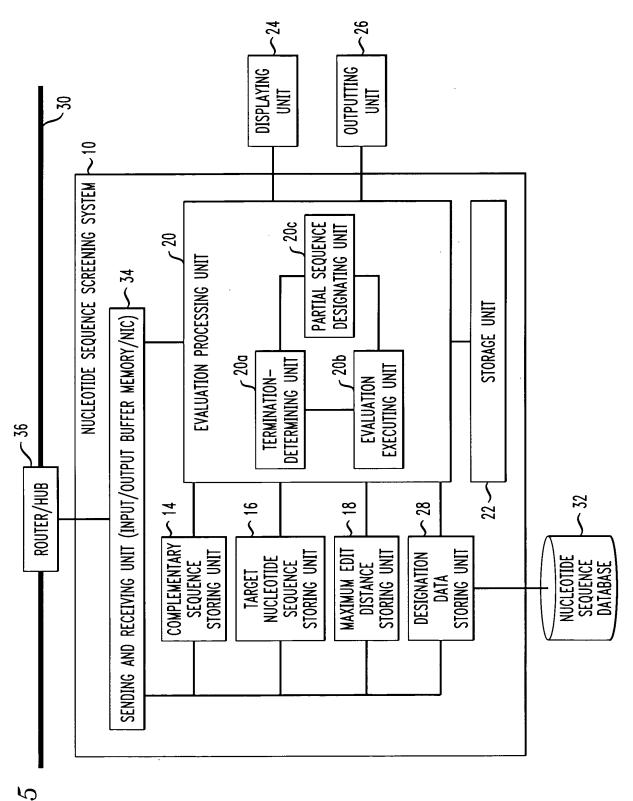
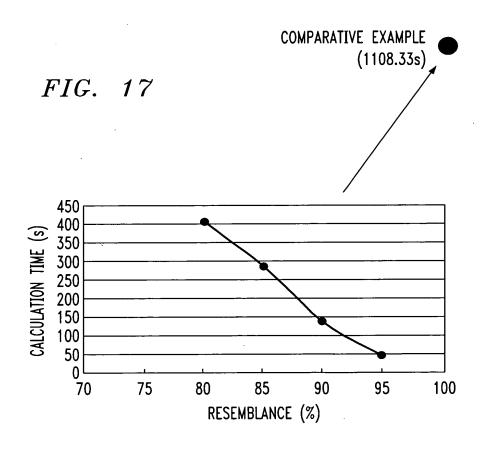


FIG. 15

FIG. 16

	EXA	COMPARATIVE EXAMPLE			
	RESEMI	Smith-Waterman			
0.80	0.85	0.90	0.95		
405.47s	284.12s	136.20s	45.05s	1108.33s	



TARGET NUCLEOTIDE SEQUENCE

PROBE SPECIFICALLY BINDING TO THE SEQUENCE